

SI guide

In the Supplementary Theory, we provide further details on the modeling approach to study cell fate in the mouse tail epidermis, as well as on the data analysis and statistics used. We start by describing how quantitative analysis of clonal data can be used to elucidate the lineage hierarchy and progenitor fate behavior under conditions of normal homeostasis. This modeling scheme and its analysis provides a platform to then consider how stem and progenitor cell fates are perturbed in the progression to basal cell carcinoma (BCC) following smoothened activation.